

Mailbox Room 12E12

U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

Office Room 12D07

SEARCH REQUEST FORM

Requestor's

Name: Anne-Marie Baker

Serial

Number: 08/963,288

Date: 8/15/02

Phone: 306-9155

Art Unit: 1632

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search: nucleic acid databases for

TTCTGA GAA

I would like the search to be size-limited to less than 30 nucleotides (in other words, I don't want any hits for sequences over 30 nucleotides).

Note: The sequence is smaller than 10 nucleotides and therefore is not subject to compliance with the sequence rules.

Point of Contact:
Barb O'Brien
Technical Information Specialist
STIC CM1 6A05 308-4291

STAFF USE ONLY

Date completed: 8-21-02

Searcher: BCB

Terminal time: 12

Elapsed time: prep 2576

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

☐ STIC

☐ CM-1

☐ Pre-S

Type of Search

☒ N.A. Sequence

☐ A.A. Sequence

☐ Structure

☐ Bibliographic

Vendors

☒ IG

☐ STN

☐ Dialog

☐ APS

☐ Geninfo

☐ SDC

☐ DARC/Questel

abs 06 Other

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 21:33:29 ; Search time 1861.18 Seconds
(without alignments)
101.193 Million cell updates/sec

Title: NA_SEQ
Perfect score: 9
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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2: gb_htg:*
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4: gb_om:*
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6: gb_pat:*
7: gb_ph:*
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14: gb_vl:*
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17: em_hum:*
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19: em_mu:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

C	1	9	100.0	15	6	AR133394	AR133394 Sequence
C	2	9	100.0	15	6	AR133395	AR133395 Sequence
C	3	9	100.0	18	6	AX277553	AX277553 Sequence
C	4	9	100.0	19	6	AR043730	AR043730 Sequence
C	5	9	100.0	19	6	AR043731	AR043731 Sequence
C	6	9	100.0	19	6	AX130312	AX130312 Sequence
C	7	9	100.0	19	6	I81958	I81958 Sequence
C	8	9	100.0	19	6	I81959	I81959 Sequence
C	9	9	100.0	20	6	A67540	A67540 Sequence
C	10	9	100.0	20	6	AR029053	AR029053 Sequence
C	11	9	100.0	20	6	AR120696	AR120696 Sequence
C	12	9	100.0	20	6	E03365	E03365 Sequence
C	13	9	100.0	22	6	AR040919	AR040919 Sequence
C	14	9	100.0	22	6	AR051826	AR051826 Sequence
C	15	9	100.0	22	6	AR115962	AR115962 Sequence
C	16	9	100.0	22	6	AR127329	AR127329 Sequence
C	17	9	100.0	22	6	AR168643	AR168643 Sequence
C	18	9	100.0	22	6	AR170236	AR170236 Sequence
C	19	9	100.0	22	6	AR171665	AR171665 Sequence
C	20	9	100.0	22	6	BD011555	BD011555 DNA mutag
C	21	9	100.0	22	6	I36216	I36216 Sequence
C	22	9	100.0	23	6	AR097057	AR097057 Sequence
C	23	9	100.0	23	6	E36223	E36223 Japanese cl
C	24	9	100.0	23	6	E47019	E47019 Simulaneol
C	25	9	100.0	24	6	A02218	A02218 Oligonucleo
C	26	9	100.0	24	6	A81021	A81021 Sequence
C	27	9	100.0	24	6	AR036118	AR036118 Sequence
C	28	9	100.0	24	6	AR136874	AR136874 Sequence
C	29	9	100.0	24	6	AX008844	AX008844 Sequence
C	30	9	100.0	24	6	AX008851	AX008851 Sequence
C	31	9	100.0	24	6	AX008852	AX008852 Sequence
C	32	9	100.0	24	6	E25644	E25644 Novel phes
C	33	9	100.0	25	6	A98319	A98319 Sequence
C	34	9	100.0	25	6	AR104820	AR104820 Sequence
C	35	9	100.0	25	6	AX027405	AX027405 Sequence
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C	38	9	100.0	26	6	AR128122	AR128122 Sequence
C	39	9	100.0	26	6	AR170508	AR170508 Sequence
C	40	9	100.0	26	6	AX080772	AX080772 Sequence
C	41	9	100.0	26	6	AX107138	AX107138 Sequence
C	42	9	100.0	26	6	AX201406	AX201406 Sequence
C	43	9	100.0	26	6	I04554	I04554 Sequence
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ALIGNMENTS

RESULT	1	AR133394	15 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	AR133394/c	Sequence 1819 from patent US 6194150.				
DEFINITION	AR133394	Sequence 1819 from patent US 6194150.				
ACCESSION	AR133394	Sequence 1819 from patent US 6194150.				
VERSION	AR133394.1	GI:14122299				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 15)					
AUTHORS	Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.					
TITLE	Nucleic acid based inhibition of CD40					
JOURNAL	Patent: US 6194150-A 1819 27-FEB-2001;					
FEATURES	location/Qualifiers					
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ORIGIN	1..15					

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
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 DB 15 TTCTGAGAA 7

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 ARI33395/C ARI33395 15 bp DNA linear PAT 16-MAY-2001
 LOCUS DEFINITION Sequence 1820 from patent US 6194150.

ACCESSION ARI33395
 VERSION ARI33395.1 GI:14122300
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)
 Unclassified.

AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.

TITLE Nucleic acid based inhibition of CD40

JOURNAL Patent: US 6194150-A 1820 27-FEB-2001;

FEATURES Location/Qualifiers

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BASE COUNT 4 a 3 c 2 g 6 t
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 AX277553 AX277553 18 bp DNA linear PAT 01-NOV-2001
 LOCUS DEFINITION Sequence 32 from Patent WO0177327.

ACCESSION AX277553
 VERSION AX277553.1 GI:16604752
 KEYWORDS

SOURCE synthetic construct.
 ORGANISM synthetic construct.

REFERENCE 1 (sites)
 Artificial sequence.

AUTHORS Carulli,J.P., Little,R.D., Becker,R.R. and Johnson,M.L.

TITLE The high bone mass gene of 11q13.3

JOURNAL Patent: WO 0177327-A 32 18-OCT-2001;

Genome Therapeutics Corporation (US)

FEATURES Location/Qualifiers

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BASE COUNT 5 a 5 c 4 g 4 t
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Query Match 100.0%; Score 9; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 LOCUS

DEFINITION Sequence 100 from patent US 5814517.
 ARO43730
 ARO43730.1 GI:5964738
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
 Unclassified.

AUTHORS Seidel,H.,Martin. and Lamb,I.,Peter.

TITLE DNA spacer regulatory elements responsive to cytokines and methods

JOURNAL Patent: US 5814517-A 100 29-SEP-1998;

for their use

FEATURES Location/Qualifiers

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BASE COUNT 4 a 5 c 4 g 6 t
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Query Match 100.0%; Score 9; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 16 TTCTGAGAA 8

RESULT 5
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 LOCUS DEFINITION Sequence 101 from patent US 5814517.

ACCESSION ARO43731
 VERSION ARO43731.1 GI:5964739
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
 Unclassified.

AUTHORS Seidel,H.,Martin. and Lamb,I.,Peter.

TITLE DNA spacer regulatory elements responsive to cytokines and methods

JOURNAL Patent: US 5814517-A 101 29-SEP-1998;

for their use

FEATURES Location/Qualifiers

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BASE COUNT 6 a 4 c 5 g 4 t
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Query Match 100.0%; Score 9; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
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 DB 8 TTCTGAGAA 16

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 LOCUS DEFINITION Sequence 1530 from Patent WO0130362.

ACCESSION AX130312
 VERSION AX130312.1 GI:14136617
 KEYWORDS

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Robbins,J.M. and Tritz,R.

TITLE Ridozyme therapy for the treatment of proliferative skin and eye

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diseases
Patent: WO 0130362-A 1530 03-MAY-2001;
JOURNAL
IMMUSOL, INC. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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/note="Cyclin A2 ribozyme binding site"
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ORIGIN

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
Db 9 TTCTGAGAA 17

RESULT 7
181958/c 181958 19 bp DNA linear PAT 10-JUN-1998
LOCUS
DEFINITION Sequence 56 from patent US 5712094.
ACCESSION 181958
VERSION 181958.1 GI:3210255
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 19)
AUTHORS Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
TITLE Methods for detecting modulators of cytokine action
JOURNAL Patent: US 5712094-A 56 27-JAN-1998;
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BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
Db 16 TTCTGAGAA 8

RESULT 8
181959 181959 19 bp DNA linear PAT 10-JUN-1998
LOCUS
DEFINITION Sequence 57 from patent US 5712094.
ACCESSION 181959
VERSION 181959.1 GI:3210256
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 19)
AUTHORS Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
TITLE Methods for detecting modulators of cytokine action
JOURNAL Patent: US 5712094-A 57 27-JAN-1998;
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6 a 4 c 5 g 4 t
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
Db 1 TTCTGAGAA 16

RESULT 9
A67540 20 bp DNA linear PAT 05-MAY-1999
LOCUS
DEFINITION Sequence 21 from Patent WO9743647.
ACCESSION A67540
VERSION A67540.1 GI:4756420
KEYWORDS
SOURCE
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 20)
AUTHORS La,T.N. and De,L.L.
TITLE DP AND E2F PROTEIN NUCLEAR LOCALISATION SIGNALS AND THEIR USE
JOURNAL MEDICAL RES COUNCIL (GB)
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BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
Db 1 TTCTGAGAA 9

RESULT 10
AR029053 20 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 21 from patent US 5859199.
ACCESSION AR029053
VERSION AR029053.1 GI:5941026
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS La,Thanhue,N.B. and de la Luna,S.
TITLE Transcription factor DP-3 and isoforms thereof
JOURNAL Patent: US 5859199-A 21 12-JAN-1999;
FEATURES
source
1..20
/organism="unknown"
BASE COUNT
7 a 3 c 4 g 6 t
ORIGIN

Query Match
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
Db 1 TTCTGAGAA 9

RESULT 11
AR120696 20 bp DNA linear PAT 16-MAY-2001
LOCUS

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DEFINITION Sequence 21 from patent US 6159691.
ACCESSION ARI20696
VERSION ARI20696.1 GI:14104272
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS La Thangue,N.D. and De la Luna,S.
TITLE Assay for a putative regulator of cell cycle progression
JOURNAL Patent: US 6159691-A 21 12-DEC-2000;
FEATURES
source
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location/Qualifiers
BASE COUNT 7 a 3 c 4 g 6 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
DB 1 TTCTGAGAA 9

RESULT 12
E03365 20 bp DNA linear PAT 29-SEP-1997
LOCUS E03365
DEFINITION Oligonucleotide for detection of human papilloma virus gene.
ACCESSION E03365
VERSION E03365.1 GI:2171582
KEYWORDS JP 1992058888-A/2.
SOURCE JP 1992058888-A/2.
ORGANISM synthetic construct.
REFERENCE
1 (bases 1 to 20)
AUTHORS Yoshie,O. and MakI,H.
TITLE OLIGONUCLEOTIDE FOR DETECTING HUMAN PAPILLOMA VIRUS GENE AND
JOURNAL DETECTION METHOD USING THE SAME
PATENT: JP 1992058888-A 2 25-FEB-1992;
SHIONOGI & CO LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992058888-A/2
PD 25-FEB-1992
PE 28-JUN-1990 JP 1990171986
PI YOSHIE OSAMU, MAKI HIDEO
PC C12N15/11,C07H21/00,C12Q1/68,G01N33/569,G01N33/574; CC
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CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
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DB 4 TTCTGAGAA 12

RESULT 13
AR040919

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LOCUS AR040919 22 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5811238.
ACCESSION AR040919
VERSION AR040919.1 GI:5961415
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Stemmer,W.P.C. and CramerI,A.
TITLE Methods for generating polynucleotides having desired
JOURNAL characteristics by iterative selection and recombination
PATENT: US 5811238-A 18 22-SEP-1998;
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|||||
DB 13 TTCTGAGAA 21

RESULT 14
AR051826 22 bp DNA linear PAT 29-SEP-1999
LOCUS AR051826
DEFINITION Sequence 18 from patent US 5830721.
ACCESSION AR051826
VERSION AR051826.1 GI:5975190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Stemmer,W.P.C. and CramerI,A.
TITLE DNA mutagenesis by random fragmentation and reassembly
JOURNAL Patent: US 5830721-A 18 03-NOV-1998;
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location/Qualifiers
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 13 TTCTGAGAA 21

RESULT 15
AR115962 22 bp DNA linear PAT 16-MAY-2001
LOCUS AR115962
DEFINITION Sequence 18 from patent US 6132970.
ACCESSION AR115962
VERSION AR115962.1 GI:14096284
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Stemmer,W.P.C.
TITLE Methods of shuffling polynucleotides
JOURNAL Patent: US 6132970-A 18 17-OCT-2000;

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FEATURES Location/Qualifiers
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 |||||
DB 13 TTCTGAGAA 21

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 22:26:44 ; Search time 206.01 Seconds
(without alignments)
75.007 Million cell updates/sec

Title: NA_SEQ
Perfect score: 9
Sequence: 1 ttctgagaa 9

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Total number of hits satisfying chosen parameters: 1662488

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	9	16	AAT14149	Cytokine responsiv
2	100.0	9	17	AAT14583	Cytokine activated
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4	100.0	9	15	AAK66325	Mouse B7-2 hammetrh
5	100.0	15	17	AAK66326	Mouse B7-2 hammetrh
6	100.0	17	21	AAF02601	Hammerhead ribozym
7	100.0	17	21	AAF02602	Hammerhead ribozym
8	100.0	17	21	AAF02603	Hammerhead ribozym
9	100.0	17	21	AA36041	Human genomic SNP

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C	15	9	100.0	19	19	AAV56841	Regulatory element
C	16	9	100.0	19	19	AAV56942	Regulatory element
C	17	9	100.0	19	21	AAAB3944	Cyclin A2 ribozyme
C	18	9	100.0	19	22	AAH59106	Cyclin A2 ribozyme
C	19	9	100.0	20	13	AAO23061	HeV-16 primer (2)
C	20	9	100.0	20	16	AAO91527	ETS-2 Mspr RTLP pr
C	21	9	100.0	20	19	AAH88330	Primer E2-A for mu
C	22	9	100.0	20	20	AAV80051	Human PM2 intron
C	23	9	100.0	20	21	AAZ45501	PCR primer used to
C	24	9	100.0	20	21	AAZ36354	PCR primer 649419-
C	25	9	100.0	21	22	AAH62317	Histamine receptor
C	26	9	100.0	21	22	AAAF7401	Primer #35. Homo
C	27	9	100.0	22	18	AAAT73036	Mutagenic PCR prim
C	28	9	100.0	22	19	AAV54907	Primer used for int
C	29	9	100.0	22	20	AAV33878	PCR primer for B6/
C	30	9	100.0	22	22	AAAD18956	PCR primer #14 to
C	31	9	100.0	23	18	AAV01403	Primer AR for dete
C	32	9	100.0	23	18	AAAT72679	PIR-related kinase
C	33	9	100.0	23	18	AAAF61980	Human ATR gene pri
C	34	9	100.0	23	19	AAAX10121	Human biatllelic po
C	35	9	100.0	23	21	AAAB8084	Citrus viroid II d
C	36	9	100.0	23	21	AAAF2057	Japanese citrus vi
C	37	9	100.0	23	21	AAZ37849	PCR primer ODH26 f
C	38	9	100.0	23	22	AAH46729	Type 11 phosphodie
C	39	9	100.0	24	18	AAAF59391	Human papilloma vi
C	40	9	100.0	24	20	AAAX57032	S. pneumoniae phes
C	41	9	100.0	24	20	AAAX36324	PCR primer used to
C	42	9	100.0	24	21	AAAX5486	Mytilus microsat
C	43	9	100.0	24	21	AAZ37061	CDNA encoding a MH
C	44	9	100.0	24	21	AAZ37068	CDNA encoding a pe
C	45	9	100.0	24	21	AAZ37069	CDNA encoding a pe

ALIGNMENTS

RESULT 1
AAT14149/c
ID AAT14149 standard; DNA; 9 BP.
XX
XX AAT14149;
XX
DT 29-MAY-1996 (first entry)
XX
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
XX
KW Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW gene transcription; inflammation; cytopenia; cancer; ss.
XX
XX
OS Synthetic.
PN WO9528482-A2.
XX
XX
PD 26-OCT-1995.
XX
XX
PF 10-APR-1995; 95WO-US04477.
XX
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
XX
PA (LIGA-) LIGAND PHARM INC.
XX
XX
PI Lamb IP, Seidel HM;
XX
XX
DR WPI; 1995-373797/48.
XX
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for

PT detecting the presence of transcriptional regulatory protein in a
sample
XX
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element
CC TTT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC activated transcriptional regulatory protein in response to a
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC spacer regulatory element can be used to detect the presence of
CC a transcriptional regulatory protein in a sample, and in assays
CC for (anti)agonists of gene transcription. The identified cpds.
CC may be used to treat cytokine-induced disease states, or to
CC ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9
|||||
DB 9 TTCTGAGAA 1

RESULT 2
AAV41583/C
ID AAV41583 standard; DNA; 9 BP.
XX
XX AAV41583;
XX
DT 04-JUN-1997 (first entry)
XX
DE Cytokine activated STAT protein dependent DNA regulatory element.
XX
XX Regulatory element; protein; cytokine; responsive; host cell;
XX transfection; agonist; antagonist; mediated; transcription;
XX modulation; STAT; STAT5; STAT6; signalling pathway; ss.
XX
OS Synthetic.
XX
XX
XX WO9630515-A1.
XX
XX 03-OCT-1996.
XX
XX 25-MAR-1996; 96WO-US04012.
XX
XX 27-MAR-1995; 95US-0411020.
XX
XX (LIGA-) LIGAND PHARM INC.
XX
XX
XX Lamb IP, Seidel HM, Tian Chan S;
XX
XX WPI: 1996-455362/45.
XX
XX
XX DNA construct for screening modulators of cytokine-mediated
XX transcription - contg. regulatory element and a cytokine-sensitive
XX promoter operably linked to a heterologous gene
XX
XX
XX Claim 5; Page 61; 72pp; English.
XX
XX A novel DNA construct comprises an oligonucleotide (ON) comprising
XX a regulatory element having the present sequence, operably linked
XX to a promoter, which is operably linked to a heterologous gene
XX (preferably a marker gene). The gene is under the transcriptional
XX control of the promoter and the ON sequence when the ON is bound by
XX a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,
XX erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,
XX IL-13 or IL-15. Cytokine responsive host cells transfected with the
XX DNA construct can be used to measure the ability of a compound to

CC act as an agonist or antagonist of cytokine mediated gene
CC transcription. In particular, they can be used to screen for
CC cytokine modulators involved in the STATs and/or STAT6 protein
CC signalling pathway.
XX
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9
|||||
DB 9 TTCTGAGAA 1

RESULT 3
AAV56876/C
ID AAV56876 standard; DNA; 9 BP.
XX
XX AAV56876;
XX
XX 02-DEC-1998 (first entry)
XX
XX
XX Regulatory element containing oligonucleotide #35.
XX
XX
XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;
XX transcriptional control; STAT protein; screening; agonist; ss.
XX
XX
XX Synthetic.
XX
XX US5814517-A.
XX
XX
XX 29-SEP-1998.
XX
XX
XX 27-MAR-1995; 95US-0410779.
XX
XX
XX 27-MAR-1995; 95US-0410779.
XX
XX PR 14-APR-1994; 94US-0228935.
XX
XX
XX (LIGA-) LIGAND PHARM INC.
XX
XX
XX Lamb IP, Seidel HM;
XX
XX
XX WPI: 1998-541763/46.
XX
XX
XX
XX DNA constructs containing cytokine-responsive regulatory elements -
XX useful in assays for transcription-regulating proteins or gene
XX transcription agonists or antagonists
XX
XX
XX Disclosure; Column 11; 58pp; English.
XX
XX
XX AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
XX production of constructs comprising a cytokine-responsive regulatory
XX element linked to a promoter which is linked to a heterologous coding
XX sequence so that the coding sequence is under the transcriptional
XX control of the regulatory element and the promoter, where the regulatory
XX element has a nucleotide sequence selected from TTGNGAA, TTANYTAA, and
XX TTGNYTAA where N is A, T, C or G, and y = 3 or 4. The constructs can be
XX used to detect or isolate transcription-regulating proteins, e.g. STAT
XX proteins, in a sample by contacting the sample with the construct so that
XX the protein binds to the regulatory element, and detecting or separating
XX the resulting complex. The cells can be used in screening assays for
XX agonists of gene transcription, in which the level of expression of the
XX coding sequence is measured in the presence and absence of a test
XX compound or in the presence of the corresponding cytokine.
XX
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttgagaa 9
 |||||
 Db 9 TTCTGAGAA 1

RESULT 4
 AAX66325/C
 ID AAX66325 standard; RNA; 15 BP.

XX AAX66325;
 AC
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Mouse B7-2 hammerhead ribozyme target SEQ ID NO:2957.

XX
 KW Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.

XX
 OS Mus sp.
 XX
 PN WO9618736-A2.
 XX
 PD 20-JUN-1996.
 XX
 PF 22-NOV-1995; 95WO-US15516.

XX
 PR 05-OCT-1995; 95US-0541365.
 PR 13-DEC-1994; 94US-0354920.
 PR 23-DEC-1994; 94US-0363253.
 PR 23-DEC-1994; 94US-0363254.
 PR 17-FEB-1995; 95US-0390850.
 PR 20-APR-1995; 95US-0426124.
 PR 02-MAY-1995; 95US-0432874.
 PR 04-MAY-1995; 95US-0434509.
 PR 07-JUL-1995; 95US-0000951.
 PR 07-JUL-1995; 95US-0000974.
 PR 07-AUG-1995; 95US-0512861.

XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper K, Gustofson J, McSwigen J, Pavco P, Stinchcomb DT;
 PI Beigelman L, Karpelsky A, Modak A, Usman N, Burgin A;
 PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
 XX
 DR WPI; 1996-300653/30.

XX
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used
 PT for the treatment of arthritis; induction of graft tolerance or
 PT treatment of auto-immune diseases
 XX
 PS Claim 10; Page 198; 307pp; English.

XX
 CC The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
 CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
 CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
 CC The ENA's can inhibit collagenase and stromelysin production in the
 CC synovial membrane of joints for the treatment or prevention of arthritis,
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for
 CC treating allergies and other inflammatory conditions. The ENA's can also
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of
 CC stromelysin without introducing the non-specific effects upon gene
 CC expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 CC is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 15 BP; 5 A; 3 C; 3 G; 4 U; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttgagaa 9
 |||||
 Db 15 TTCTGAGAA 7

RESULT 5
 AAX66326/C
 ID AAX66326 standard; RNA; 15 BP.

XX AAX66326;
 AC
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Mouse B7-2 hammerhead ribozyme target SEQ ID NO:2958.

XX
 KW Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.

XX
 OS Mus sp.
 XX
 PN WO9618736-A2.
 XX
 PD 20-JUN-1996.
 XX
 PF 22-NOV-1995; 95WO-US15516.

XX
 PR 05-OCT-1995; 95US-0541365.
 PR 13-DEC-1994; 94US-0354920.
 PR 23-DEC-1994; 94US-0363253.
 PR 23-DEC-1994; 94US-0363254.
 PR 17-FEB-1995; 95US-0390850.
 PR 20-APR-1995; 95US-0426124.
 PR 02-MAY-1995; 95US-0432874.
 PR 04-MAY-1995; 95US-0434509.
 PR 07-JUL-1995; 95US-0000951.
 PR 07-JUL-1995; 95US-0000974.
 PR 07-AUG-1995; 95US-0512861.

XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper K, Gustofson J, McSwigen J, Pavco P, Stinchcomb DT;
 PI Beigelman L, Karpelsky A, Modak A, Usman N, Burgin A;
 PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
 XX
 DR WPI; 1996-300653/30.

XX
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used
 PT for the treatment of arthritis; induction of graft tolerance or
 PT treatment of auto-immune diseases
 XX
 PS Claim 10; Page 198; 307pp; English.

XX
 CC The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
 CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
 CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
 CC The ENA's can inhibit collagenase and stromelysin production in the
 CC synovial membrane of joints for the treatment or prevention of arthritis,
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance


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KM interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
DR WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 76; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the C/EBP displacement
CC protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 other;

Query Match          100.0%; Score 9; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||||
Db 13 TTCTGAGAA 5

RESULT 9
AAA36041
ID AAA36041 standard; DNA: 17 BP.
AC AAA36041;
XX
XX 26-JUL-2000 (first entry)
DT
XX
DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:98.
XX
XX Human: single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW genomic classification; identification; DNA fingerprinting;
KW tumour characterisation; hybridisation; ss.
XX
OS Homo sapiens.
XX
PN WO200018960-A2.
XX
PD 06-APR-2000.
XX
PF 24-SEP-1999; 99WO-US22283.
XX
PR 25-SEP-1998; 98US-0101757.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Landers JE, Jordan B, Housman DE, Charest A;

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XX
DR WPI; 2000-293181/25.
XX
XX Detection of single nucleotide polymorphisms in genomes by preparation
PT and analysis of reduced complexity genomes, useful for genotyping,
PT fingerprinting and determining allele frequency of SNPs -
XX
XX Disclosure; Page 56; 111pp; English.
XX
XX A method has been developed for detecting the presence or absence of a
CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC method comprises preparing a reduced complexity genome (RCG) from the
CC genomic sample and analysing the RCG for the presence or absence of a
CC SNP allele. The method can be used to characterise a tumour, to generate
CC a genomic pattern for an individual genome or to generate a genomic
CC classification code for a genome. The method can be used to assess
CC whether a subject is at risk for developing a disease or to identify a
CC set of SNP alleles associated with a disease. The method can also be
CC used to perform linkage analysis. AAA35944 to AAA35947 represent
CC sequences used in the exemplification of the present invention. AAA35948
CC to AAA36632 represent nucleotide sequences containing SNPs.
XX
SQ Sequence 17 BP; 4 A; 1 C; 4 G; 8 T; 0 other;

Query Match          100.0%; Score 9; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||||
Db 1 ttctgagaa 9

RESULT 10
AAV24227/C
ID AAV24227 standard; DNA: 18 BP.
XX
XX AAV24227;
AC
XX
XX 12-AUG-1998 (first entry)
DT
XX
XX Primer alpha(1)a for human alphoid DNA sequence.
DE
XX
XX CENP-B box; mammalian artificial chromosome; MAC; chromosome 21;
KW mammalian telomere; centromere; yeast artificial chromosomes; YAC;
KW somatic gene therapy; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX Homo sapiens.
XX
XX WO9808964-A1.
XX
XX 05-MAR-1998.
PD
XX
XX 26-AUG-1996; 96WO-JP02381.
PF
XX
XX 26-AUG-1996; 96WO-JP02381.
PR
XX
XX (KENO/) IKENO M.
PA (MASU/) MASUMOTO H.
PA (OKAZ/) OKAZAKI T.
XX
XX Cooke HJ, Grimes BR, Ikeno M, Masumoto H, Okazaki T;
PI WPI; 1998-216941/19.
XX
XX Mammalian artificial chromosomes - prepared using DNA construct
PT comprising mammalian telomere and centromere containing copies of
PT CENP-B box sequences
XX
XX Disclosure; Page 34; 95pp; English.
XX

```

XX	RESULT 11
XX	AAV24228
XX	ID AAV24228 standard; DNA; 18 BP.
XX	AAV24228;
XX	12-AUG-1998 (first entry)
XX	Primer alpha(1)b for human alphoid DNA sequence.
XX	CENP-B box; mammalian artificial chromosome; MAC; chromosome 21;
XX	KW mammalian telomere; centromere; yeast artificial chromosomes; YAC;
XX	somatic gene therapy; PCR primer; ss.
XX	Synthetic.
XX	OS Homo sapiens.
XX	WO9808964-A1.
XX	05-MAR-1998.
XX	26-AUG-1996; 96WO-JP02381.
XX	26-AUG-1996; 96WO-JP02381.
XX	(KENO/) IKENO M.
XX	PA (MASU/) MASUMOTO H.
XX	PA (OKAZ/) OKAZAKI T.
XX	Cooke HJ, Grimes BR, Ikono M, Masumoto H, Okazaki T;
XX	WPI; 1998-216941/19.
XX	Mammalian artificial chromosomes - prepared using DNA construct
XX	comprising mammalian telomere and centromere containing copies of
XX	CENP-B box sequences
XX	Disclosure: Page 34; 95pp; English.
XX	This sequence is a primer for a human alphoid DNA sequence that can be

CC	RESULT 12
CC	ABAB82604
CC	ABAB82604 standard; DNA; 18 BP.
CC	XX
CC	XX
CC	AC
CC	ABAB82604;
CC	XX
CC	XX
CC	DT
CC	25-JAN-2002 (first entry)
CC	XX
CC	XX
CC	DE
CC	HBW1 polymorphism containing amplicon PCR primer 1863F.
CC	XX
CC	XX
CC	Human; high bone mass; HBW gene; Zmax1 gene; chromosome 11; 11q13.3;
CC	KW
CC	sequence tagged site; SRS; osteoporosis; osteopathic; gene therapy;
CC	KW
CC	antiassess therapy; vaccine; bone disorder; Paget's disease; adapter;
CC	XX
CC	sclerostosis; osteomacrolacta; fibrous dysplasia; PCR primer; linker; ss.
CC	XX
CC	OS
CC	Homio sapiens.
CC	OS
CC	Synthetic.
CC	XX
CC	XX
CC	PN
CC	WO200177327-A1.
CC	XX
CC	PD
CC	18-OCT-2001.
CC	XX
CC	XX
CC	21-JUN-2000; 2000WO-US16951.
CC	PP
CC	05-APR-2000; 2000US-0543771.
CC	PR
CC	05-APR-2000; 2000US-0544398.
CC	PR
CC	XX
CC	PA
CC	(GENO-) GENOME THERAPEUTICS CORP.
CC	XX
CC	XX
CC	Carulli JP, Little RD, Recker RR, Johnson ML;
CC	PI
CC	WPI; 2001-657171/75.
CC	DR
CC	XX
CC	XX
CC	PT
CC	New high bone mass (HBW) and Zmax1 genes and proteins useful for
CC	modulating bone mass for the treatment of e.g. osteoporosis -
CC	XX
CC	PS
CC	Disclosure; Page 63; 443pp; English.
CC	XX
CC	XX
CC	The present invention describes the human Zmax1 gene and the high bone
CC	mass (HBW) gene, which are found on chromosome 11q13.3. The Zmax1 and
CC	HBW genes have osteopathic activities. The genes can be used in gene
CC	therapy.

CC therapy, antisense therapy and in the production of vaccines. They
 CC can be used in the diagnosis and treatment of bone disorders including
 CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous
 CC dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent
 CC sequences used in the exemplification of the present invention.

XX
 SQ Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 9; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
 |||||
 Db 6 ttctgagaa 14

RESULT 13

ABA82646
 ID ABA82646 standard; DNA; 18 BP.

AC ABA82646;

DT 25-JAN-2002 (first entry)

DE Human Zmax1 PCR primer SEQ ID NO:32.

XX Human: high bone mass; HBM gene; Zmax1 gene; chromosome 11: 11q13.3;

KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;

KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;

KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.

XX Homo sapiens.

OS Synthetic.

XX MO200177327-A1.

XX 18-OCT-2001.

XX 21-JUN-2000; 2000MO-US16951.

XX 05-APR-2000; 2000US-0543771.

XX 05-APR-2000; 2000US-0544398.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Carulli JP, Little RD, Recker RR, Johnson ML;

XX WPI; 2001-657171/75.

XX New high bone mass (HBM) and Zmax1 genes and proteins useful for

XX modulating bone mass for the treatment of e.g. osteoporosis -

XX disclosure; Page 103; 443pp; English.

XX The present invention describes the human Zmax1 gene and the high bone

XX mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and

XX HBM genes have osteopathic activities. The genes can be used in gene

XX therapy, antisense therapy and in the production of vaccines. They

XX can be used in the diagnosis and treatment of bone disorders including

XX osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous

XX dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent

XX sequences used in the exemplification of the present invention.

XX Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Db 6 ttctgagaa 14
 |||||

RESULT 14

AA741612/C
 ID AA741612 standard; DNA; 19 BP.

AC AA741612;

DT 04-JUN-1997 (first entry)

DE Oligonucleotide containing core DNA regulatory element.

XX Regulatory element; SPAT; protein; cytokine; responsive;

KW host cell; transfection; agonist; antagonist; mediated; STAT5;

KW transcription; modulation; signalling pathway; SPAT6;

KW oligonucleotide; electrophoretic mobility shift assay; EMSA; ds.

XX Synthetic.

OS Synthetic.

XX MO9630515-A1.

XX 03-OCT-1996.

XX 25-MAR-1996; 96MO-US04012.

XX 27-MAR-1995; 95US-0411020.

XX (LIGA-) LIGAND PHARM INC.

XX Lamb IP, Seidel HM, Tian Chan S;

XX WPI; 1996-455362/45.

XX DNA construct for screening modulators of cytokine-mediated

XX transcription - conty. regulatory element and a cytokine-sensitive

XX promoter operably linked to a heterologous gene

XX Example 1; Page 26; 72pp; English.

XX A novel DNA construct comprises the present oligonucleotide (ON),

XX which contains a core a regulatory element, operably linked to a

XX promoter, which is operably linked to a heterologous gene

XX (preferably a marker gene). The gene is under the transcriptional

XX control of the promoter and the ON sequence when the ON is bound by

XX a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,

XX erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,

XX IL-13 or IL-15. Cytokine responsive host cells transfected with the

XX DNA construct can be used to measure the ability of a compound to

XX act as an agonist or antagonist of cytokine mediated gene

XX transcription. In particular, they can be used to screen for

XX cytokine modulators involved in the STAT5 and/or STAT6 protein

XX signalling pathway

XX following an electrophoretic mobility shift assay the DNA construct

XX was found to bind IL-4 and IL-13 moderately.

SQ Sequence 19 BP; 4 A; 5 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
 |||||
 Db 16 TTCTGAGAA 8

```

RESULT 15
AAV56941/C
ID AAV56941 standard; DNA; 19 BP.
XX
AC AAV56941;
XX
DT 02-DEC-1998 (first entry)
XX
DE Regulatory element containing oligonucleotide #100.
XX
KM Cytokine-responsive regulatory; primer; promoter; detection; isolation;
XX transcriptional control; STAT protein; screening; agonist; ss.
XX
OS Synthetic.
XX
PN US5814517-A.
XX
PD 29-SEP-1998.
XX
PF 27-MAR-1995; 95US-0410779.
XX
PR 27-MAR-1995; 95US-0410779.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb 1P, Seidel HM;
XX
DR WPI: 1998-541763/46.
XX
PT DNA constructs containing cytokine-responsive regulatory elements -
PT useful in assays for transcription-regulating proteins or gene
PT transcription agonists or antagonists
XX
PS Example 1; Column 19-20; 58pp; English.
XX
CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
CC production of constructs comprising a cytokine-responsive regulatory
CC element linked to a promoter which is linked to a heterologous coding
CC sequence so that the coding sequence is under the transcriptional
CC control of the regulatory element and the promoter, where the regulatory
CC element has a nucleotide sequence selected from TTCNCGAA, TTANYTAA, and
CC TTCTGTAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be
CC used to detect or isolate transcription-regulating proteins, e.g. STAT
CC proteins, in a sample by contacting the sample with the construct so that
CC the protein binds to the regulatory element, and detecting or separating
CC the resulting complex. The cells can be used in screening assays for
CC agonists of gene transcription, in which the level of expression of the
CC coding sequence is measured in the presence and absence of a test
CC compound or in the presence of the corresponding cytokine.
XX
SQ Sequence 19 BP; 4 A; 5 C; 4 G; 6 T; 0 other;

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Query Match 100.0%; Score 9; DB 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ttctgagaa 9
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DB 16 TTCTGAGAA 8

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Search completed: August 20, 2002, 23:27:54
 Job time: 3670 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 22:19:24 ; Search time 43.04 Seconds
(without alignments)
51.364 Million cell updates/sec

Title: NA_SEQ
Perfect score: 9
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 403436

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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5: /cgn2_6/pdata2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/pdata2/1na/beckfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	9	100.0	9	1 US-08-411-020-13	Sequence 13, Appl
2	9	100.0	9	1 US-08-369-796-34	Sequence 34, Appl
3	9	100.0	9	1 US-08-410-779B-35	Sequence 35, Appl
4	9	100.0	9	2 US-08-852-091-34	Sequence 34, Appl
5	9	100.0	9	5 PCT-US95-04477-35	Sequence 35, Appl
6	9	100.0	9	5 PCT-US95-17025-34	Sequence 34, Appl
7	9	100.0	15	2 US-08-585-684B-1819	Sequence 1819, Ap
8	9	100.0	15	2 US-08-585-684B-1820	Sequence 1820, Ap
9	9	100.0	15	4 US-09-038-073-1819	Sequence 1819, Ap
10	9	100.0	15	4 US-09-038-073-1820	Sequence 1820, Ap
11	9	100.0	19	1 US-08-411-020-56	Sequence 56, Appl
12	9	100.0	19	1 US-08-411-020-57	Sequence 57, Appl
13	9	100.0	19	1 US-08-410-779B-100	Sequence 100, Appl
14	9	100.0	19	1 US-08-410-779B-101	Sequence 101, Appl
15	9	100.0	19	5 PCT-US95-04477-100	Sequence 100, App
16	9	100.0	19	5 PCT-US95-04477-101	Sequence 101, App
17	9	100.0	20	2 US-08-723-415B-21	Sequence 21, Appl
18	9	100.0	20	3 US-09-078-317-7	Sequence 7, Appl1
19	9	100.0	20	3 US-08-600-882-20	Sequence 20, Appl
20	9	100.0	20	3 US-09-189-627A-21	Sequence 21, Appl
21	9	100.0	20	5 PCT-US94-10261A-20	Sequence 20, Appl
22	9	100.0	22	1 US-08-198-431-18	Sequence 18, Appl
23	9	100.0	22	1 US-08-564-955-18	Sequence 18, Appl
24	9	100.0	22	2 US-08-537-874-18	Sequence 18, Appl
25	9	100.0	22	3 US-08-929-140-13	Sequence 13, Appl
26	9	100.0	22	3 US-08-621-859-18	Sequence 18, Appl
27	9	100.0	22	3 US-09-100-856A-18	Sequence 18, Appl

28	9	100.0	22	4 US-09-075-511-18	Sequence 18, Appl
29	9	100.0	22	4 US-09-099-015-18	Sequence 18, Appl
30	9	100.0	22	4 US-09-232-863-18	Sequence 18, Appl
31	9	100.0	22	4 US-09-560-579A-13	Sequence 13, Appl
32	9	100.0	22	4 US-09-133-508A-18	Sequence 18, Appl
33	9	100.0	22	4 US-09-165-060-18	Sequence 18, Appl
34	9	100.0	22	4 US-09-501-698-18	Sequence 18, Appl
35	9	100.0	22	4 US-09-590-778-18	Sequence 18, Appl
36	9	100.0	23	3 US-09-067-284-2	Sequence 2, Appl1
37	9	100.0	24	2 US-08-953-041-4	Sequence 4, Appl1
38	9	100.0	24	4 US-09-159-417-4	Sequence 4, Appl1
39	9	100.0	25	3 US-08-781-891-39	Sequence 39, Appl
40	9	100.0	25	3 US-08-781-891-141	Sequence 141, App
41	9	100.0	25	3 US-08-912-272-70	Sequence 70, Appl
42	9	100.0	25	4 US-09-026-039-70	Sequence 70, Appl
43	9	100.0	26	1 US-08-379-078-553	Sequence 553, App
44	9	100.0	26	1 US-08-379-078-558	Sequence 558, App
45	9	100.0	26	1 US-08-379-078-663	Sequence 663, App

ALIGNMENTS

RESULT 1
US-08-411-020-13/c
Sequence 13, Application US/08411020
Patent No. 5712094
GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ligand Pharmaceuticals Incorporated
STREET: 9393 Towne Centre Drive
City: San Diego
STATE: California
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,020
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jurgensen, Thomas E.
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0030.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
SYNTHETIC DNA"
US-08-411-020-13

Query Match 100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  ttctgagaa 9
          |||||
DB       9  TTCTGAGAA 1

RESULT  2
US-08-369-796-34/C
; Sequence 34, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA synthetic probe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-369-796-34

Query Match      100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ttctgagaa 9
          |||||
DB       9  TTCTGAGAA 1

RESULT  3
US-08-410-779B-35/C
; Sequence 35, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
STREET: 9393 TOWNE CENTRE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
US-08-410-779B-35

Query Match      100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ttctgagaa 9
          |||||
DB       9  TTCTGAGAA 1

RESULT  4
US-08-852-091-34/C
; Sequence 34, Application US/08852091
; Patent No. 5863228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA synthetic probe
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-852-091-34

Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
|||||
Db 9 TTCTGAGAA 1

RESULT 5
PCT-US95-04477-35/c
Sequence 35, Application PC/TUS9504477
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 165
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/228,935
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
SYNTHETIC DNA"
PCT-US95-04477-35

Query Match 100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
|||||
Db 9 TTCTGAGAA 1

RESULT 6
PCT-US95-17025-34/c
Sequence 34, Application PC/TUS9517025
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17025
FILING DATE: 28-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA synthetic probe
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-17025-34

Query Match 100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
|||||
Db 9 TTCTGAGAA 1

RESULT 7
US-08-585-684B-1819/c
Sequence 1819, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Slinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751

```

CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1819:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1819

Query Match      100.0%; Score 9; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ttctagaa 9
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Db 15 TTCTGAGAA 7

RESULT 8
US-08-585-684B-1820/c
Sequence 1820, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: MCSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1820:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1820
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APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1820:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1820

Query Match      100.0%; Score 9; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 TTCTGAGAA 4

RESULT 9
US-09-038-073-1819/c
Sequence 1819, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: MCSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1819:
SEQUENCE CHARACTERISTICS:
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LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-1819

Query Match 100.0%; Score 9; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9
|||||
Db 15 TTCTGAGA 7

RESULT 10
US-09-038-073-1820/C
Sequence 1820, Application US/09038073
Patent No. 6194150

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1820:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-1820

Query Match 100.0%; Score 9; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9
|||||
Db 12 TTCTGAGA 4

RESULT 11
US-08-411-020-56/C
Sequence 56, Application US/08411020
Patent No. 5712094

GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ligand Pharmaceuticals Incorporated
STREET: 9393 Towne Centre Drive
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,020
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jurgensen, Thomas E.
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0030.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
SYNTHETIC DNA"
US-08-411-020-56

Query Match 100.0%; Score 9; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9
|||||
Db 16 TTCTGAGA 8

RESULT 12
US-08-411-020-57
Sequence 57, Application US/08411020
Patent No. 5712094
GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ligand Pharmaceuticals Incorporated
STREET: 9393 Towne Centre Drive
CITY: San Diego
STATE: California
COUNTRY: US

```
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,020
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jurgensen, Thomas E.
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0030.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-411-020-57
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 tctctgagaa 9
    |||
DB 8 TTCTGAGAA 16
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RESULT 13
US-08-410-779B-100/C
; Sequence 100, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
```

```
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-410-779B-100
```

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Query Match 100.0%; Score 9; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 tctctgagaa 9
    |||
DB 16 TTCTGAGAA 8
```

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RESULT 14
US-08-410-779B-101
; Sequence 101, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-410-779B-101
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Query Match 100.0%; Score 9; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ttctgagaa 9
|||||
Db 8 TTCTGAGAA 16

RESULT 15
PCT-US95-04477-100/c
; Sequence 100, Application PC/TUS9504477
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 165
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; PCT-US95-04477-100

Query Match 100.0%; Score 9; DB 5; Length 19;
Best local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
|||||
Db 16 TTCTGAGAA 8

Search completed: August 20, 2002, 23:24:06
Job time: 3882 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 21:26:14 ; Search time 1559.67 Seconds
(without alignments)
77.884 Million cell updates/sec

Title: NA_SEQ
Perfect score: 9
Sequence: 1 tctcgagaa 9

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 28088

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_estli:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	29	12	AZ818898 2M0089N11
2	8	88.9	29	12	AZ313531 1M0029N07
3	8	88.9	20	12	AZ303578 1M0003H07
4	8	88.9	24	12	AZ819888 2M0091H18
5	8	88.9	26	12	AZ313876 1M0030H21
6	8	88.9	27	12	AZ387860 1M0147M20
7	8	88.9	28	12	AZ648296 1M0517E15
8	8	88.9	30	12	AZ514561 1M0361N07
9	8	82.2	19	12	AZ399220 1M0164P23
10	7	82.2	19	12	AZ810627 2M0076H17
11	7	82.2	19	12	AZ833621 1M0129L21
12	7	82.2	20	12	AZ468141 1M0281D04
13	7	82.2	21	12	AZ360212 1M0103K04
14	7	82.2	22	12	AZ430664 1M0215D17
15	7	82.2	22	12	AZ457101 1M0260J17
16	7	82.2	22	12	AL475949 T. brucei
17	7	82.2	23	12	AZ388663 1M0148J15

18	7	82.2	23	12	AZ424145 1M0203P03
19	7	82.2	24	12	AZ343358 1M0076A18
20	7	82.2	24	12	AZ357286 1M0098B15
21	7	82.2	24	12	AZ446127 1M0242F19
22	7	82.2	24	12	AZ579569 1M0367L12
23	7	82.2	24	12	AZ596086 1M0409E07
24	7	82.2	24	12	AZ596086 1M0409E07
25	7	82.2	25	10	D19996
26	7	82.2	26	12	AZ514399 1M0361K01
27	7	82.2	26	12	AZ602086 1M0420K07
28	7	82.2	27	12	AZ778941 2M0014E09
29	7	82.2	28	9	AU012291
30	7	82.2	28	12	AZ346840 1M0082G16
31	7	82.2	28	12	AZ609297 1M034B06
32	7	82.2	28	12	TA108D080
33	7	82.2	29	12	AZ818898 2M0089N11
34	7	82.2	29	12	AZ852213 2M0154P16
35	7	82.2	30	12	AZ510129 1M0354L24
36	7	77.8	19	12	AZ473867 1M0290K06
37	7	77.8	19	12	AZ489350 1M0321K14
38	7	77.8	20	12	AZ489135 1M0319H15
39	7	77.8	20	12	AZ780925 2M0018A16
40	7	77.8	20	12	AZ782243 2M0022B21
41	7	77.8	20	12	AZ626828 2M0102P15
42	7	77.8	21	12	AZ488178 1M0318M13
43	7	77.8	21	12	AZ595078 1M0407A03
44	7	77.8	21	12	AZ806440 2M0068B05
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ALIGNMENTS

RESULT 1
AZ818898 29 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0089N11F Mouse 10kb plasmid UUGCIW library Mus musculus genomic
DEFINITION Clone UUGC2M0089N11 F, DNA sequence.
ACCESSION AZ818898
VERSION AZ818898.1 GI:12988806
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus; 1 (bases 1 to 29)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0089 row: N column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089N11"
/clone_lib="Mouse 10kb plasmid UUGCIW library"

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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

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BASE COUNT      12 a      8 c      4 g      5 t
ORIGIN
Query Match      100.0%; Score 9; DB 12; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ttctgaga 9
    |||||
Db 9 TCTGAGAA 17

```

```

RESULT 2
LOCUS      A2313531      19 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION 1M0029N07 Mouse 10kb plasmid UGCG1M library Mus musculus genomic
ACCESSION  A2313531
VERSION    A2313531.1 GI:10358522
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0029 row: N column: 07
            Seq primer: CACACAGCAACACCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
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            1..19
            /organism="Mus musculus"
            /strain="C57BL/6J"
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            /clone="UGCG1M0029N07"

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/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

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BASE COUNT      6 a      2 c      5 g      6 t
ORIGIN
Query Match      88.9%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2 tctgaga 9
    |||||
Db 8 TCTGAGAA 15

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RESULT 3
LOCUS      A2303578      20 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION 1M0003H07F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
ACCESSION  A2303578
VERSION    A2303578
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0003 row: H column: 07
            Seq primer: CGTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES
            source
            1..20
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"

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/clone="UUGC1M003H07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (q114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
8 a 2 c 3 g 7 t

Query Match
Best Local Similarity 100.0%; Score 8; DB 12; Length 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 tctgaga 9
|||||||
Db 10 TCTGAGA 17

RESULT 4
A2819888 24 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0091H18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0091H18 R, DNA sequence.
ACCESSION
A2819888
VERSION
A2819888.1 GI:12989796
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: H column: 18
Seq primer: CACACAGGAACACGACATACAC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. 24
/organism="Mus musculus"
/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="UUGC2M0091H18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (q114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
6 a 5 c 5 g 8 t

Query Match
Best Local Similarity 100.0%; Score 8; DB 12; Length 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgaga 8
|||||||
Db 14 TTCTGAGA 21

RESULT 5
A2313876 26 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION 1M0030H21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0030H21 F, DNA sequence.
ACCESSION
A2313876
VERSION
A2313876.1 GI:10359208
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0030 row: H column: 21
Seq primer: CCGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M030H21"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (911473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      6 a      6 c      9 g      5 t
ORIGIN

```

```

Query Match      88.9%; Score 8; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 tctcgaga 8
    |||||
Db 8 TCTCGAGA 1

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RESULT 6
LOCUS      A2387860      27 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION IM0147M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  A2387860
VERSION     A2387860.1 GI:10501568
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 27)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
             M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
             University of Utah Genome Center
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0147 row: M column: 20
             Seq primer: CACACAGCAACACCTATGACC
             Class: plasmid ends
             High quality sequence stop: 27.
             Location/Qualifiers
             1..27

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147M20"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (911473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      8 a      3 c      7 g      9 t
ORIGIN

```

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Query Match      88.9%; Score 8; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 2 tctcgaga 9
    |||||
Db 4 TCTGAGA 11

```

```

RESULT 7
LOCUS      A2648296      28 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION IM0517E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  A2648296
VERSION     A2648296.1 GI:11780621
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 28)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
             M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
             University of Utah Genome Center
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0517 row: E column: 15
             Seq primer: CGTGTAAACGACGCGCAGT
             Class: plasmid ends
             High quality sequence stop: 28.
             Location/Qualifiers

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FEATURES
Source

FEATURES

source 1. 28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M031N07"
/clone_1ib="Mouse 10kb plasmid U081M 1library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 11 a 7 c 4 g 6 t
ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctgagaa 9
|||||||
Db 17 TCTGAGAA 24

RESULT 8
A2514561 30 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0361N07F Mouse 10kb plasmid U081M 1library Mus musculus genomic
DEFINITION clone U081M0361N07 F, DNA sequence.
ACCESSION A2514561
VERSION A2514561.1 GI:10695793
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: N column: 07
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.

JOURNAL
COMMENT

FEATURES
source Location/Qualifiers
1. 30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M0361N07"
/clone_1ib="Mouse 10kb plasmid U081M 1library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 2 c 10 g 5 t
ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctgagaa 9
|||||||
Db 3 TCTGAGAA 10

RESULT 9
A2399220 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0164P23R Mouse 10kb plasmid U081M 1library Mus musculus genomic
DEFINITION clone U081M0164P23 R, DNA sequence.
ACCESSION A2399220
VERSION A2399220.1 GI:10514292
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0164 row: P column: 23
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends

JOURNAL
COMMENT

High quality sequence stop: 19.

FEATURES
Location/Qualifiers

source
1..19
/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCGCM0164P23"

/clone_11b="Mouse 10kb plasmid UUCGCM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114[gb]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
4 a 2 c 4 g 9 t

ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.2e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttcttgagaa 9

DB 6 TTCTGTAGTA 14

RESULT 10

A2810627/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp DNA linear GSS 20-FEB-2001
2M0076H17F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
clone UUCG2M0076H17 F, DNA sequence.
A2810627
A2810627.1 GI:12978066
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
Islam,H., Longace,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: H column: 17
Seq primer: CGTTCTAAACGACGCCACGT

Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers

source
1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0076H17"

/clone_11b="Mouse 10kb plasmid UUCGCM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114[gb]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
6 a 5 c 1 g 7 t

ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.2e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttcttgagaa 9

DB 15 TTATGTAGAA 7

RESULT 11

A2835621

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp DNA linear GSS 20-FEB-2001
2M0129L2R Mouse 10kb plasmid UUCGCM library Mus musculus genomic
clone UUCG2M0129L21 R, DNA sequence.
A2835621
A2835621.1 GI:13005529
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
Islam,H., Longace,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: L column: 21

Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0129L21"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 3 c 3 g 7 t

ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.2e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
Db 2 TTCTGTGAA 10

RESULT 12

LOCUS

AZ468141 20 bp DNA linear GSS 04-OCT-2000

DEFINITION IM0281D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0281D04 F, DNA sequence.

ACCESSION AZ468141
VERSION AZ468141.1 GI:10626266

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

JOURNAL COMMENT

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Plate: 0281 Row: D Column: 04
Seq primer: CCGTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0281D04"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 0 c 4 g 9 t

ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.2e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
Db 7 TTATGAGAA 15

RESULT 13

LOCUS

AZ360212 21 bp DNA linear GSS 02-OCT-2000

DEFINITION IM0103K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0103K04 F, DNA sequence.

ACCESSION AZ360212
VERSION AZ360212.1 GI:10473912

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

JOURNAL COMMENT

Unpublished (2000)

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Unpublished (2000)

Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: K column: 04
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

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/strain="C57BL/6J"
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/clone="U06C1M0103K04"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 7 c 5 g 3 t

ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ttctagaa 9
||||| 111
Db 7 TTCTGGAA 15

RESULT 14

AZ430664

LOCUS

AZ430664 22 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0215D17F Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C1M0215D17 F, DNA sequence.

ACCESSION

AZ430664

VERSION

AZ430664.1 GI:10554677

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE

1

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

AUTHORS

M.

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JOURNAL

Unpublished (2000)

COMMENT

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University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0215 row: D column: 17
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source

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/clone="U06C1M0215D17"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 4 c 3 g 9 t

ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 22;
Best Local Similarity 88.9%; Pred. No. 7.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ttctagaa 9
||||| 111
Db 13 TTCTGGAA 21

RESULT 15

AZ457101/c

AZ457101 22 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0260J17F Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C1M0260J17 F, DNA sequence.

ACCESSION

AZ457101

VERSION

AZ457101.1 GI:10615226

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE

1

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

AUTHORS

M.

TITLE

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JOURNAL

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COMMENT

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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0260 row: j column: 17
 Seq primer: CGTGTGAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

source

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 /clone="U0GC1M0260J17"
 /clone_11b="Mouse 10kb plasmid U0GC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b1AF128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 2 g 6 t
 ORIGIN

Query Match

82.2%; Score 7.4; DB 12; Length 22;

Best Local Similarity 88.9%; Pred. No. 7.3e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
 || |||||
 Db 15 TTTGAGAA 7

Search completed: August 20, 2002, 22:51:42
 Job time: 5128 sec

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